

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$$

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

Input file T81: Output File T811.pat
Sequence length 979

	M	A	G	S	P		5
GAATTCGGCAGGAGCCAGCCAGTCCGCCG/MCGRRGCCCGGCTCCCTGGGGCAGC	ATG	GCG	GGG	TGG	CCG		72
L L W G P R A G G V G L L V L L L L G L							25
CTG CTC TGG GGG CCG CCG GCC GGG GGC GTC GGC CTT TTG GTG CTG CTG CTG CTC GGC CTG							132
F R P P P A L C A R P V K E P R G L S A							45
TTT CCG CCG CCC CCC GCG CTC TGC GCG CCG CCG GTA AAG GAG CCC CCG GGC CTA AGC GCA							192
A S P P L A E T G A P R R F R R S V P R							65
GCG TCT CCG CCC TTG GCT GAG ACT GGC GCT CTT CCG CCG TTC CCG CCG TCA GTG CCC CGA							252
G E A A G A V Q E L A R A L A H L L E A							85
GGT GAG GCG GCG GGG GCG GTG CAG GAG CTG GCG CCG GCG CTG GCG CAT CTG CTG GAG GCC							312
E R Q E R A R A E A Q E A E D Q Q A R V							105
GAA CGT CAG GAG CCG GCG CCG GCC GAG GCG CAG GAG GCT GAG GAT CAG CAG GCG CCG GTC							372
L A Q L L R V W G A P R N S D P A L G L							125
CTG CCG CAG CTG CTG CCG GTC TGG GGC GCC CCC CCG AAC TCT GAT CCG GCT CTG GGC TTG							432
D D D P D A P A A Q L A R A L L R A R L							145
GAC GAC GAC CCC GAC GCG CCT GCA GCG CAG CTC GCT CCG GCT CTG CTC CCG GCC CCG CTT							492
D P A A L A A Q L V P A P V P A A A L R							165
GAC CCT GCG GCC CTA GCA GCC CAG CTT GTC CCC GCG CCC GTC CCC GCG GCG GCG CTC CGA							552
P R P P V Y D D G P A G P D A E E A G D							185
CCC CCG CCC CCG GTC TAC GAC GAC GGC CCC CCG GGC CCG GAT GCT GAG GAG GCA GGC GAC							612
E T P D V D P E L L R Y L L G R I L A G							205
GAG ACA CCC GAC GTG GAC CCC GAG CTG TTG AGG TAC TTG CTG GGA CCG ATT CTT GCG GGA							672
S A D S E G V A A P R R L R R A A D H D							225
AGC GCG GAC TCC GAG GGG GTG GCA GCC CCG CCG CCG CTC CCG CGT GCC GCC GAC CAC GAT							732
V G S E L P P E G V L G A L L R V K R L							245
GTG GGC TCT GAG CTG CCC CCT GAG GGC GTG CTG GGG GCG CTG CTG CGT GTG AAA CCG CTA							792
E T P A P Q V P A R R L L P P *							261
GAG ACC CCG GCG CCC CAG GTG CCT GCA CCG CCG CTC TTG CCA CCC TGA							840
GCACGCCCGGATCCCGTGCCAGCCTGGGACCCAGAAGTGCCCCCGCCATCCCGCCACGAGCTGCTCCCCCGCCAGCAC							919
GTCCAGAGCAACTTACCCCGGCCAGCCAGCCCTCTCACCCGAGGATCCCTACCCCTGGC							979

FIG. 2

Fig 3

Percent Similarity:

by: 29.412

T79	1	MLAG	47
D45913	1	MARLSTGKAAC.QVVLGLLITSLTESSILTSECPQLCVCEIRPWF	44
T79	48	AVLCHRKRFRVAVPEGIPTETRLLDLGKNRIKTLNQDEFAS	87
D45913	45	TPQSTYREATTVDCNDLRLTRIPGNLSSDTQVLLQLQSNNI	84
T79	88	FPHLEELELNENIVSAVEPGAFFNNLFLNRLTLGLRSNRLKLIPLGVFTGLS	137	
D45913	85	AKTVDELQQLFNLTEDFSQNNFTNIKEVGLANLT	119
T79	138	NLTKLDTRENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRAFSGLNSL	187	
D45913	120	QLTTLHLEENQISEMTDYCLQDLSNLQELYINHNOISTISANAFSGLKNL	169	
T79	188	EQLTLEKCNLTISIPTALSHLHGLIVLRLRLNLINAIARDYSFKRLYRLKV	237	
D45913	170	LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENFVIGILDMNFRPLSNLRS	219	
T79	238	LEISHWPYLDTMTFNCYGLN.LTSLSIHCNLTAVPYLAVRHLVYLRFL	286	
D45913	220	LVLAG.MYLTDPVGNALVGLDSLESLSFYDNKLIKVPQALQKVPNLKFL	268	
T79	287	NLSYNPISTIEGSMHELLRLQEIQLVG.GQLAVVEPY	323	
D45913	269	DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELTKLE	318	
T79	324	AFRGLNYLRLVNLVSGNQLTTLEESVFSVGNLETIL	360
D45913	319	ATMNPKLSYIHLAFRSVPALSLMLNNALNAVYQKTVESLPNLREISI	368	
T79	361	DSNPLACDCRLLWFRRLNFRNRQPT.CATPEFVQGKEFKDFPDVLL	409	
D45913	369	HSNPLRCDCVIHWINSNKTNIHFMEPLSMFCAMPPEYRGQVK...EVLI	415	
T79	410	PNYFT.CRRARIRDRKAQVVFVDEGHTVQFVCRADGDPFPAWLSPRKH	458	
D45913	416	QDSSEQCLPMISHDTFPNHLNMDIGTTLFLDCRAMAEPEPEIYWVTPIGN	465	
T79	459	LVSAS.NGRLTVPDGTLEVRYAQVQDNGTYLCIAANAGGNDSPAHLLH	507	
D45913	466	KITVETLSDKYKLSSEGTLLEIANIQIEDSGRYTCVAQNVQADTRVATIK	515	
T79	508	V.....	RSYSPDWPHQ	518
D45913	516	VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN	565	
T79	519	PNKTF.....	AFISNQPGEGEANSTRA	540

FIG. 3 (1 of 2)

FOOD" 6850350



FIG. 4

T	R	P	I	L	V	I	H	D	E	Q	K	G	P	E	V	T	S	N		19
CC	ACG	CGT	CCG	ATC	TTG	GTC	ATC	CAC	GAT	GAA	CAG	AAG	GGG	CCG	GAA	GTG	ACC	TCC	AAT	59
A	A	L	T	L	R	N	F	C	N	W	Q	K	Q	H	N	P	P	S	D	39
GCT	GCC	CTC	ACT	CTG	CGG	AAC	TTT	TGC	AAC	TGG	CAG	AAG	CAG	CAC	AAC	CCA	CCC	AGT	GAC	119
R	D	A	E	H	Y	D	T	A	I	L	F	T	R	Q	D	L	C	G	S	59
CGG	GAT	GCA	GAG	CAC	TAT	GAC	ACA	GCA	ATT	CTT	TTG	ACC	AGA	CAG	GAC	TTG	TGT	GGG	TCC	179
Q	T	C	D	T	L	G	M	A	D	V	G	T	V	C	D	P	S	R	S	79
CAG	ACA	TGT	GAT	ACT	CTT	GGG	ATG	GCT	GAT	GTT	GGA	ACT	GTG	TGT	GAT	CCG	AGC	AGA	AGC	239
C	S	V	I	E	D	D	G	L	Q	A	A	F	T	T	A	H	E	L	G	99
TGC	TCC	GTC	ATA	GAA	GAT	GAT	GGT	TTA	CAA	GCT	GCC	TTG	ACC	ACA	GCC	CAT	GAA	TTA	GGC	299
H	V	F	N	M	P	H	D	D	A	K	Q	C	A	S	L	N	G	V	N	119
CAC	GTG	TTT	AAC	ATG	CCA	CAT	GAT	GAT	GCA	AAG	CAG	TGT	GCC	AGC	CTT	AAT	GGT	GTG	AAC	359
Q	D	S	H	M	M	A	S	M	L	S	N	L	D	H	S	Q	P	W	S	139
CAG	GAT	TCC	CAC	ATG	ATG	GCG	TCA	ATG	CTT	TCC	AAC	CTG	GAC	CAC	AGC	CAG	CCT	TGG	TCT	419
P	C	S	A	Y	M	I	T	S	F	L	D	N	G	H	G	E	C	L	M	159
CCT	TGC	AGT	GCC	TAC	ATG	ATT	ACA	TCA	TTT	CTG	GAT	AAT	GGT	CAT	GGG	GAA	TGT	TTG	ATG	479
D	K	P	Q	N	P	I	Q	L	P	G	D	L	P	G	T	S	Y	D	A	179
GAC	AAG	CCT	CAG	AAT	CCC	ATA	CAG	CTC	CCA	GGC	GAT	CTC	CCT	GGC	ACC	TGC	TAC	GAT	GCC	539
N	R	Q	C	Q	F	T	F	G	E	D	S	K	H	C	P	D	A	A	S	199
AAC	CGG	CAG	TGC	CAG	TTT	ACA	TTT	GGG	GAG	GAC	TCC	AAA	CAC	TGC	CCT	GAT	GCA	GCC	AGC	599
T	C	S	T	L	W	C	T	G	T	S	G	G	V	L	V	C	Q	T	K	219
ACA	TGT	AGC	ACC	TTG	TGG	TGT	ACC	GGC	ACC	TCT	GGT	GGG	GTG	CTG	GTG	TGT	CAA	ACC	AAA	659
H	F	P	W	A	D	G	T	S	C	G	E	G	K	W	C	I	N	G	K	239
CAC	TTG	CCG	TGG	GCG	GAT	GGC	ACC	AGC	TGT	GGA	GAA	GGG	AAA	TGG	TGT	ATC	AAC	GGC	AAG	719
C	V	N	K	T	D	R	K	H	F	D	T	P	F	H	G	S	W	G	M	259
TGT	GTG	AAC	AAA	ACC	GAC	AGA	AAG	CAT	TTT	GAT	ACG	CCT	TTT	CAT	GGA	AGC	TGG	GGA	ATG	779
W	G	P	W	G	D	C	S	R	T	C	G	G	G	V	Q	Y	T	M	R	279
TGG	GGG	CCT	TGG	GGA	GAC	TGT	TGG	AGA	ACG	TGC	GGT	GGA	GGA	GTG	CAG	TAC	ACG	ATG	AGG	839
E	C	D	N	P	V	P	K	N	G	G	K	Y	C	E	G	K	R	V	R	299
GAA	TGT	GAC	AAC	CCA	GTC	CCA	AAG	AAT	GGA	GGG	AAG	TAC	TGT	GAA	GGC	AAA	CCA	GTG	CGC	899
Y	R	S	C	N	L	E	D	C	P	D	N	N	G	K	T	F	R	E	E	319
TAC	AGA	TCC	TGT	AAC	CTT	GAG	GAC	TGT	CCA	GAC	AAT	AAT	GGA	AAA	ACC	TTT	AGA	GAG	GAA	959

FIG. 5 (1 of 3)

P D S T S V C V Q G Q C V K A G C D R I	399
CCA GAT TCC ACC TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CCC ATC	1199
I D S K K K F D K C G V C G G N G S T C	419
ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TGC GGG GGA AAT GGA TCT ACT TGT	1259
K K I S G S V T S A K P G Y H D I I T I	439
AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT GGA TAT CAT GAT ATC ATC ACA ATT	1319
P T G A T N I E V K Q R N Q R G S R N N	459
CCA ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT	1379
G S F L A I K A A D G T Y I L N G D Y T	479
GGC AGC TTT CTT GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT	1439
L S T L E Q D I M Y K G V V L R Y S G S	499
TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG TAC AGC GGC TCC	1499
S A A L E R I R S F S P L K E P L T I Q	519
TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT CTC AAA GAG CCC TTG ACC ATC CAG	1559
V L T V G N A L R P K I K Y T Y F V K K	539
GTT CTT ACT GTG GGC AAT GCC CTT CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG	1619
K K E S F N A I P T F S A W V I E E W G	559
AAG AAG GAA TCT TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC	1679
E C S K T C G K G Y K K R S L K C L S H	579
GAA TGT TCT AAG ACC TGT GGG AAG GGT TAC AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT	1739
D G G V L S H E S C D P L K K P K H F I	599
GAT GGA GGG GTG TTA TCT CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA	1799
D F C T M A E C S *	609
GAC TTT TGC ACA ATG GCA GAA TGC AGT TAA	1829
GTGGTTTAAGTGGTGTGCTCTGAGGGCAAGGCCAAAGTGAGGAAGGGCTGGTGCAGGGAAAGCAAGAAGGCTGGAGGG	1908
ATCCAGCGTATCTTGCCAGTAACCAAGTGAGGTGTATCAGTAAGGTGGGATTATGGGGGTAGATAGAAAAGGAGTTGAAT	1987
CATCAGAGTAAGTCCAGTTCGCAATTTGATAGGATAGTTAGTGAGGATTATTAACCTCTGAGCAGTGATATAGCATA	2066
ATAAAGCCCCGGGCATTATTATTATTATTTCTTTTGTACATCTATTACAAGTTTAGAAAAAACAAGCAATTGTCAAA	2145
AAAAGTTAGAACTATTACAACCCCTGTTTCCTGGTACTTATCAAATACTTAGTATCATGGGGGTGGGAAATGAAAAGT	2224
AGGAGAAAAGTGAGATTTTACTAAGACCTGTTTACTTTACCTCACTAACAATGGGGGGAGAAAGGAGTACAAATAGGA	2303
TCTTTGACCAGCACTGTTTATGGCTGCTATGGTTTCAGAGAATGTTTATACATTATTTCTACCGAGAATTAAAACTTCA	2382
GATTGTTCAACATGAGAGAAAGGCTCAGCAACGTGAAATAACGCCAAATGGCTTCCTCTTTCTTTTGGACCATCTCA	2461
GTCTTTATTGTGTAATTCATTTTGAGGAAAAACAACCTCCATGTATTTATTCAAGTGCATTAAGTCTACAATGGAAA	2540
AAAAGCAAGTGAAGCATTAGATGCTGGTAAAAGCTAGAGGAGACACAATGAGCTTAGTACCTCCAACCTTCCTTTCTTTCC	2619
TACCATGTAACCTGCTTTGGGAATATGGATGTAAAGAAGTAACTTGTGTCTCATGAAAATCAGTACAATCACACAAGG	2698

FIG. 5 (2 f 3)

AGGATGAAACGCCCGGAACAAAAATGAGGTGTGTAGAACAGGGTCCCAAGGTTTTGGGACATTGAGATCACTTGTCTTG 2777
 TGGTGGGGAGGCTGCTGAGGGGTAGCAGGTCCATCTCCAGCAGCTGGTCCAACAGTCGTATCCTGGTGAATGTCTGTC 2856
 AGCTCTTCTGTGAGAATATGATTTTTTCCATATGTATATAGTAAATATGTTACTATAAATTACATGTACTTTATAAGT 2935
 ATTGGTTTGGGTGTTCCTTCCCAAGAAGGACTATAGTTAGTAATAAATGCCTATAATAACATATTTATTTTATACATT 3014
 ATTTCTAATGAAAAAACTTTTAAATTATATCGCTTTTGTGGAAGTGCCATATAAATAGAGTATTTATACAATATATGT 3093
 TACTAGAAATAAAAGAACACTTTTGGAAAAAAGGGCGGCCGC 3147

TGGTGGGGAGGCTGCTGAGGGGTAGCAGGTCCATCTCCAGCAGCTGGTCCAACAGTCGTATCCTGGTGAATGTCTGTC

TANGO 71/ADAMTS-1 Comparison (90% Protein Sequence Identity)

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251 DQSMADFHGSGGLKHYLLTLFSVAARFYKHPsirnsislVVVKILVTYEEQ 300
      ||||:|
1 .....TRPILVTHDEQ 11

301 KGPEVTSNAALTLRNFCSWQKQHNPSDRDPEHYDTAILFTRODLGSGHT 350
      |||||:|
12 KGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRODLGSGQT 61

351 CDTLGMADVGTVCDPSSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKH 400
      |||||:|
62 CDTLGMADVGTVCDPSSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAQ 111

401 CASLNGVSGDSHLMASMLSSLDHSQFWSPCSAYMVTSLDNGHGECIMDK 450
      |||||:|
112 CASLNGVQDSHMTASMLSNLDHSQFWSPCSAYMITSLDNGHGECIMDK 161

451 PQNPILKPSDLPGTLYDANRQCQFTFGEEKHCPDAASTCTTLWCTGTSG 500
      ||||:|
162 PQNPILQPGDLPGTLYDANRQCQFTFGEDSKHCPDAASTCTTLWCTGTSG 211

501 GLLVCQTKHFPWADGTSCGEGKWCVSGKCVNKTDMKHFATPVHGSWGPWG 550
      |||||:|
212 GVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTDRKHFDTPFHGSWGPWG 261

551 PWGDCSRTCCGGVQYTMRECDNFPVPRNGGKYCEGRVRYRSCNIEDCPDN 600
      |||||:|
262 PWGDCSRTCCGGVQYTMRECDNFPVPRNGGKYCEGRVRYRSCNIEDCPDN 311

601 NGKITFREEQCEAHNEFSKASFGNEPTVEMTPKYAGVSPKDRCKLTCEARG 650
      |||||:|
312 NGKITFREEQCEAHNEFSKASFGSGPAVENIPKYAGVSPKDRCKLICQARG 361

651 IGYFFVLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKKFDRKGV 700
      |||||:|
362 IGYFFVLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKKFDRKGV 411

701 CGGNGSTCKKMSGIVTSTRPGYHDIVTIPAGATNIEVKHRNQGRSRNGS 750
      |||||:|
412 CGGNGSTCKKISGSVTSAPKPGYHDIITPTGATNIEVKQRNQGRSRNGS 461

751 FLAIRAADGTYILNGNFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 800
      |||||:|
462 FLAIRAADGTYILNGDYTLSTLEQDIMYKGVVLRYSGSSAALERIRSFSP 511

801 LKEPLTIQVLMVGHALRPKIKFTYFMKKTESFNAIPTFSEWIEEWGEC 850
      |||||:|
512 LKEPLTIQVLTVGVALRPKIKYTFVKKKTESFNAIPTFSAWIEEWGE. 560

901 WSPCKTCGKGYKRTLKCVSHDGGVLSNESCDPLKKPKHYIDFCTLTC 950
      |||||:|
561 ...CSKTCGKGYKRSCLKLSHDGGVLSHESCDPLKKPKHYIDFCTMAEC 607

951 S* 951
      |
608 S* 609

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FIG. 6

gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg	50
Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu	
1 5 10	
atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt	98
Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly	
15 20 25 30	
acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa	146
Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Glu	
35 40 45	
tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc	194
Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys	
50 55 60	
act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct	242
Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro	
65 70 75	
tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc	290
Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly	
80 85 90	
aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat	338
Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His	
95 100 105 110	
gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt	386
Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys	
115 120 125	
ggt ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca	434
Gly Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro	
130 135 140	
aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc	482
Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser	
145 150 155	
tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag	530
Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu	
160 165 170	
gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat	578
Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn	
175 180 185 190	
gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tcg cca aag	626
Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys	
195 200 205	

Fig. 7 (1 of 4)

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc	674
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe	
210 215 220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct	722
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser	
225 230 235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc	770
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg	
240 245 250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga	818
Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly	
255 260 265 270	
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga	866
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg	
275 280 285	
ccc ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att	914
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile	
290 295 300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt	962
Gln Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe	
305 310 315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc	1010
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe	
320 325 330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta	1058
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu	
335 340 345 350	
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt	1106
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser	
355 360 365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct	1154
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala	
370 375 380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aag aca gag	1202
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu	
385 390 395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg	1250
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp	
400 405 410	

Fig. 7 (2 of 4)

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg 1298
 Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val
 415 420 425 430

cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa 1346
 Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu
 435 440 445

gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac 1394
 Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His
 450 455 460

tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt 1442
 Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly
 465 470 475

tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta 1490
 Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu
 480 485 490

tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538
 Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp
 495 500 505 510

ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg 1592
 Phe Cys Thr Leu Thr Gln Cys Ser
 515

ggaaggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa 1652
 gcagtgaggt gtggcaagga ggtgtgtgta ggggatacat agcaaaggag gtagatcagg 1712
 aactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa 1772
 gacatacag agcactaagg agcccaaaag cactattagt atctcttttc ttatatctat 1832
 cgcacaaata attttcagag tctggcagaa gccctgttgc actgtactaa ctagatactt 1892
 ctatcacaa agattgggaa aggcacaagca gaaagatggg aagactgggt ttcaaacaag 1952
 gcttggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc 2012
 gctgggttgc gtggttttac ggaagggttga tgcattcatt ctatcaacag tgaaaagtgc 2072
 agcttggttca acgtgacaga aaggctcatc tccgtgaaag agctcctgat ttcttcttac 2132
 accatctcag ttcttaacta tagttcatgt tgaggtagaa acaattcatc tatttataaa 2192
 atgtacattg gaaaaaaaaa gtgaagttta tgaggtacac ataaaaactg aaggaaacaa 2252
 tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgaggtt 2312
 gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgt gccagagtta 2372
 gaatggggta tagagatcag ggtcccatga gatgggggaa atggtgatca ctcatctcac 2432
 atgggaggct gctgcagggt agcagggtcca ctctggcag ctggtccaac agtcgtatcc 2492
 tggatgaatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtatat 2552
 gtatatagta aaatatgtta ctatgaattg catgtacttt ataagtattg gtgtgtctgt 2612
 tccttctaag aaggactata gtttataata aatgcctata ataacatatt tatttttata 2672
 catttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732
 atagagtatt tatacaatat atgttaacta gaaataataa agaacactt ttgaatgtgt 2792
 atgcctattt tctggagtgg gattaacttc tgggcaagaa atctgatgag acacaaacat 2852
 tggacttcaa gacagtttta aattttgggt aaatgaactg tatttctgtt ttatagacgt 2912
 actaataaaa aagaagttga tgatgtcttt agtggttaaga ttgttactaa tgtggttggc 2972
 aaattgctgt aaagagccag atagtaagca tttatggcat tgtaggctat ctttctgcc 3032
 acaaccatgt gacagtgagt gctttgtagg actgagagca gccataaatg acatgtaaat 3092

Fig. 7 (3 of 4)

gataaactgt ggctgtgctt taataaaact ttatttacaa aaaaaaaaaa aaa

3145

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

ttc agc ggc ctc aac agc ctg gaa cag ctg acg ctg gag aaa tgc aat	928
Phe Ser Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn	
190 195 200	
ctg acc tcc atc ccc acg gag gcg ctc tcc cac ctg cac ggc ctc atc	976
Leu Thr Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile	
205 210 215	
gtc ctg cgg cta cga cat ctc aac atc aat gcc atc agg gac tac tcc	1024
Val Leu Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser	
220 225 230	
ttc aag agg ctg tac cga ctt aag gtc tta gag atc tcc cac tgg ccc	1072
Phe Lys Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro	
235 240 245 250	
tac ctg gac acc ata acc ccc cgg acg cgt ggg tcg ac	1110
Tyr Leu Asp Thr Ile Thr Pro Arg Thr Arg Gly Ser	
255 260	

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

ctcttgatg tgcgcagccg cagagcgtg ctgctgtgcc taatacccat cgctgcgcac 60
 ttgacagcca gtccgcccgt ccggagcccg gctcgttggg gcagc atg gcg ggg tcg 117
 Met Ala Gly Ser
 1

ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg 165
 Pro Leu Leu Cys Gly Pro Arg Ala Gly Gly Val Gly Ile Leu Val Leu
 5 10 15 20

ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc 213
 Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
 25 30 35

gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag 261
 Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
 40 45 50

acg agc act ccc ctc cgc ttg cgt cgg gcc gtg ccc cga gga gag gcg 309
 Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
 55 60 65

ggg ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag 357
 Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
 70 75 80

gag gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat 405
 Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
 85 90 95 100

cag cag gcg cgt gtc ctg gcg cag ctg ctg cgc gcc tgg ggc tct ccg 453
 Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
 105 110 115

cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca 501
 Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Asp Pro Asp Ala Pro
 120 125 130

gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc 549
 Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
 135 140 145

ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg 597
 Pro Gln Cys Met Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
 150 155 160

gcg acg aga ctc ctg acg tgg acc ctg agc tgc tgaggtactt gctagggcgg 650
 Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
 165 170 175

atcctcaccg gaagttcggg gccagaggct gctcctgccc cgcgccgcct ccgccgatct 710
 gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactgggggc tctgctacgc 770
 gtcaaacgcc tggagaaccc ctcgccccag gcgcgggcac gccgcctcct gcctccctga 830

Fig. 9 (1 of 2)

